

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/541,427
Source: PU/10
Date Processed by STIC: 11/7/05

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RAW SEQUENCE LISTING

DATE: 11/07/2005

PATENT APPLICATION: US/10/541,427

TIME: 09:31:22

Input Set : A:\Sequence List.txt

Output Set: N:\CRF4\11072005\J541427.raw

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3 <110> APPLICANT: Zelinski, Thomas
4     Kessler, Maria
5     Hauer, Bernhard
7 <120> TITLE OF INVENTION: METHODS FOR PRESERVING AND/OR STORING CELLS HAVING A NITRILASE
8     OR NITRILE HYDRATASE AVTIVITY
10 <130> FILE REFERENCE: 12810-00105-US
-> 12 <140> CURRENT APPLICATION NUMBER: US/10/541,427
-> 12 <141> CURRENT FILING DATE: 2005-07-05
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014880
13 <151> PRIOR FILING DATE: 2003-12-24
15 <150> PRIOR APPLICATION NUMBER: DE 103 00 500.5
16 <151> PRIOR FILING DATE: 2003-01-08
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1071
24 <212> TYPE: DNA
25 <213> ORGANISM: Alcaligenes faecalis
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1068)
30 <223> OTHER INFORMATION: coding for nitrilase
32 <400> SEQUENCE: 1
33 atg cag aca aga aaa atc gtc cgg gca gcc gcc gta cag gcc gcc tct 48
34 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
35 1 5 10 15
36 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
37 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
38 20 25 30
39 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
40 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
41 35 40 45
42 tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192
43 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
44 50 55 60
45 tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac 240
46 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
47 65 70 75 80
48 agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att 288
49 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
50 85 90 95
51 ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg 336
52 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu

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53	100	105	110	
54 ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384			
55 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg				
56 115 120 125				
57 aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432			
58 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr				
59 130 135 140				
60 gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct	480			
61 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala				
62 145 150 155 160				
63 cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac	528			
64 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr				
65 165 170 175				
66 tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta	576			
67 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu				
68 180 185 190				
69 tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc	624			
70 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala				
71 195 200 205				
72 tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc	672			
73 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser				
74 210 215 220				
75 agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac	720			
76 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His				
77 225 230 235 240				
78 aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg	768			
79 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala				
80 245 250 255				
81 ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc	816			
82 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly				
83 260 265 270				
84 ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg	864			
85 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala				
86 275 280 285				
87 atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg	912			
88 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu				
89 290 295 300				
90 gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa	960			
91 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys				
92 305 310 315 320				
93 agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att	1008			
94 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile				
95 325 330 335				
96 gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg	1056			
97 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val				
98 340 345 350				
99 caa gag ccg tct tga	1071			
100 Gln Glu Pro Ser				
101 355				

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103 <210> SEQ ID NO: 2

104 <211> LENGTH: 356

105 <212> TYPE: PRT

106 <213> ORGANISM: *Alcaligenes faecalis*

108 <400> SEQUENCE: 2

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109 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser
110   1           5           10           15
111 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
112           20           25           30
113 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
114           35           40           45
115 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
116           50           55           60
117 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
118           65           70           75           80
119 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
120           85           90           95
121 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
122           100          105          110
123 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
124           115          120          125
125 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
126           130          135          140
127 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
128           145          150          155          160
129 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
130           165          170          175
131 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
132           180          185          190
133 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
134           195          200          205
135 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
136           210          215          220
137 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
138           225          230          235          240
139 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
140           245          250          255
141 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
142           260          265          270
143 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
144           275          280          285
145 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
146           290          295          300
147 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
148           305          310          315          320
149 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
150           325          330          335
151 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
152           340          345          350

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153 Gln Glu Pro Ser

154 355

VERIFICATION SUMMARY

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12 M:270 C: Current Application Number differs, Replaced Current Application No

12 M:271 C: Current Filing Date differs, Replaced Current Filing Date